

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2002, 10:08:05 ; Search time 1866.06 Seconds  
(without alignments)  
5607.145 Million cell updates/sec

Title: US-09-743-194-4

Perfect score: 500  
Sequence: 1 ggaagctcgtctacagcagc9.....tacgtttatacatacat 500

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_da: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_com: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_to: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htgo\_inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
------------	-------	--------------------	----	-------------

1	497	99.4	1400	8	SCYOL110W	Z74852 S.cerevisia
2	497	99.4	44019	8	SCCHRXY44	Z48149 S.cerevisia
3	404	80.8	1541	8	SCYOL109W	Z74851 S.cerevisia
4	160	32.0	848	11	CNS0618W	AL399990 T7 end of
5	141	28.2	1671	6	SCU18313	U18313 Saccharomyc
6	73.4	14.7	7218	6	I66494	166494 Sequence 14
7	66.2	13.2	156550	2	AC015830	AC015830 Homo sapi
8	65.2	13.0	143585	2	AC013349	AC013349 Homo sapi
9	65	13.0	52359	2	AC010772	AC010772 Homo sapi
10	64	12.8	64789	2	AC083839	AC083839 Homo sapi
11	63.6	12.7	867	11	CNS06K84	AL403274 T7 end of
12	63.6	12.7	6668	6	AX346599	AX346599 Sequence
13	63.6	12.7	196502	2	AL359957	AL359957 Homo sapi
14	63.4	12.7	83440	2	AC024285	AC024285 Homo sapi
15	63	12.6	8087	2	AC106848	AC106848 Homo sapi
16	63	12.6	70511	2	AC091083	AC091083 Homo sapi
17	62.8	12.6	81120	2	AC022851	AC022851 Homo sapi
18	62.2	12.4	56693	2	AC084077	AC084077 Homo sapi
19	62	12.4	7058	6	AX348438	AX348438 Sequence
20	62	12.4	14006	6	AX346860	AX346860 Sequence
21	62	12.4	72386	2	AC102703	AC102703 Mus muscu
22	62	12.4	179902	2	AP003630	AP003630 Oryza sat
23	62	12.4	231972	2	AC068055	AC068055 Homo sapi
24	61.8	12.4	4587	9	HS3337540	AL3337540 Homo sapi
25	61.8	12.4	63365	2	AC087168	AC087168 Homo sapi
26	61.8	12.3	56857	2	AC087437	AC087437 Homo sapi
27	61.6	12.3	56857	2	AC021917	AC021917 Homo sapi
28	61.6	12.2	6070	6	AX281468	AX281468 Sequence
29	61.2	12.2	6070	6	AX346581	AX346581 Sequence
30	61.2	12.2	6070	6	AX348804	AX348804 Sequence
31	61.2	12.2	131271	2	AC015927	AC015927 Homo sapi
32	61	12.2	749	9	HS3336745	AL336745 Homo sapi
33	60.8	12.2	78227	2	AC067768	AC067768 Homo sapi
34	60.6	12.1	349980	6	AX344566	AX344566 Sequence
35	60.4	12.1	6668	6	AX346598	AX346598 Sequence
36	60.4	12.1	99263	2	CNS01DX9	AL139177 Homo sapi
37	60.4	12.1	125876	2	AC026380	AC026380 Mus muscu
38	60.4	12.1	181413	2	AC023818	AC023818 Homo sapi
39	60.2	12.0	64767	2	AC102701	AC102701 Mus muscu
40	60.2	12.0	66240	2	AC090633	AC090633 Homo sapi
41	60.2	12.0	71751	2	AC090222	AC090222 Homo sapi
42	60.2	12.0	74119	2	AC036177	AC036177 Homo sapi
43	60	12.0	60565	2	AC023852	AC023852 Homo sapi
44	59.6	11.9	9539	6	AX277889	AX277889 Sequence
45	59.6	11.9	9539	6	AX323566	AX323566 Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS SCYOL110W 1400 bp DNA linear PLN 11-AUG-1997  
DEFINITION S.cerevisiae chromosome XV reading frame ORF YOL110W.  
ACCESSION Z74852 Y13140  
VERSION Z74852.1 GI:1419976  
KEYWORDS  
SOURCE  
ORGANISM  
baker's yeast.  
Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
REFERENCE  
1 (bases 1 to 1400)  
AUTHORS Durand,P., Hliger,F., Portetelle,D. and Vandenbol,M.  
JOURNAL Unpublished  
REFERENCE  
2 (bases 1 to 1400)  
AUTHORS MIPS  
JOURNAL MIPS  
TITLE Direct Submission  
JOURNAL Submitted (04-JUL-1996) Data collected by MIPS on behalf of the  
European yeast chromosome XV sequencing project. MIPS at the  
Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152  
Martinsried, FRG; E-mail: Mewes@mips.emblnet.org  
FEATURES  
source  
1. 1400





REFERENCE  
AUTHORS  
JOURNAL  
REFERENCE  
AUTHORS  
JOURNAL  
TITLE

Enkhayrta, Fungal: Ascomycota: Sacccharomycotina: Sacccharomycetes  
Sacccharomycetales: Sacccharomycetaceae: Sacccharomyces.  
Durand P., Hilgert F.F., Portetelle, D. and Vandenbol, M.  
Unpublished  
2 (bases 1 to 1541)  
MIPS.  
Direct Submission  
Submitted (04-JUL-1996) Data collected by MIPS on behalf of the

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/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/chromosome="XV"
408. .749
CDS

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Query Match 80.8%; Score 404; DB 8; Length 1541;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

gtagccacagatbatttttggatataccaaatgaagttcttaccacattatattat  
ttaaagcgtgggttatggagtcacacaggccttatcggttttatnccatgacgcat  
gtgcctccagtgatttttggatnaccatgaagtttctaaccaattttatattat  
accttgaatnagtcgagttcgtctcgtatctcgtcgtcttctgtaggtctctc

LOCUS	DEFINITION	RESULT 4
CNS0618W	848 bp	DNA
CNS0618W	17 end of clone AS0AA018G01 of library AS0AA from strain CLB 53	linear
		STS 10-JAN-2001

REFERENCE  
AUTHORS  
TITLE

1 (bases 1 to 848)  
Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P.,  
Aigle, M., and Durrens, P.  
Genomic Exploration of the Hemiascomycetous Yeasts: 5.  
Eukaryota: Fungi, Ascomycota: saccharomycotina: saccharomycetes.  
Saccharomycetales: Saccharomycetaceae: Saccharomyces.

DELOUNTIS, FAKKADAKIS, BOU, B., BROUETTES, C., CASARAGOLIS, de-Montigny, J., Dujon, B., Durieux, P., Lepingle, A., Llorente, B., Malperuy, A., Neuvéglise, C., Ozler-Kalogopoulos, O., Potter, S., Saurin, W., Tekak, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Winkler, P. and Weissbach, J.

PUBLISHED 11/3/2010  
 REFERENCE 3 (pages 1 to 848)  
 AUTHORS Genoscope.  
 TITLE Genoscope.  
 DIRECT SUBMISSION Direct Submission  
 JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage,  
 2, rue Gustave Courbet, 91067 Evry cedex, FRANCE (ev-maj) .  
 2, rue Gustave Courbet, Evry Cedex, FRANCE (ev-maj) .

FEATURES  
SOURCE

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1. 848
   /organism="Saccharomyces bayanus"
   /strain="CLIB 533"
   /variety="varium"
   /db_xref="taxon:4931"
   /clone="AS0AA018G01"
   /clone_lib="AS0AA"

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Query Match	32.0%	Score 160	DB 11	Length 848
Best Local Similarity	69.6%	Prod. No. 66-29		
Matches 277	Conservative	1	Mismatches 106	Indels 14
				Gaps 4

  

Accession	Score	Length	Identical	Similarity	Accession	Score	Length	Identical	Similarity
1	99	848	100	100	1	99	848	100	100
94	66	848	99	99	94	66	848	99	99
61	61	848	99	99	61	61	848	99	99
154	61	848	99	99	154	61	848	99	99
121	61	848	99	99	121	61	848	99	99
214	61	848	99	99	214	61	848	99	99
181	61	848	99	99	181	61	848	99	99
272	61	848	99	99	272	61	848	99	99
241	61	848	99	99	241	61	848	99	99
322	61	848	99	99	322	61	848	99	99
301	61	848	99	99	301	61	848	99	99
382	61	848	99	99	382	61	848	99	99
361	61	848	99	99	361	61	848	99	99
440	61	848	99	99	440	61	848	99	99

  

Accession	Score	Length	Identical	Similarity	Accession	Score	Length	Identical	Similarity
1	99	848	100	100	1	99	848	100	100
94	66	848	99	99	94	66	848	99	99
61	61	848	99	99	61	61	848	99	99
154	61	848	99	99	154	61	848	99	99
121	61	848	99	99	121	61	848	99	99
214	61	848	99	99	214	61	848	99	99
181	61	848	99	99	181	61	848	99	99
272	61	848	99	99	272	61	848	99	99
241	61	848	99	99	241	61	848	99	99
322	61	848	99	99	322	61	848	99	99
301	61	848	99	99	301	61	848	99	99
382	61	848	99	99	382	61	848	99	99
361	61	848	99	99	361	61	848	99	99
440	61	848	99	99	440	61	848	99	99

  

Accession	Score	Length	Identical	Similarity	Accession	Score	Length	Identical	Similarity
1	99	848	100	100	1	99	848	100	100
94	66	848	99	99	94	66	848	99	99
61	61	848	99	99	61	61	848	99	99
154	61	848	99	99	154	61	848	99	99
121	61	848	99	99	121	61	848	99	99
214	61	848	99	99	214	61	848	99	99
181	61	848	99	99	181	61	848	99	99
272	61	848	99	99	272	61	848	99	99
241	61	848	99	99	241	61	848	99	99
322	61	848	99	99	322	61	848	99	99
301	61	848	99	99	301	61	848	99	99
382									

	BASE COUNT	369 a	359 c	442 g	501 t	GMRNLSGILLDMKTCGLMSWVGLPILLSRVFESIALRQYVAQLNSPGLLHERGVRL VLPRSGSLSDIVPEPRPK
	ORIGIN					
	Query Match	28.2%;	Score 141;	DB 8;	Length 1671;	
	Best Local Similarity	100.0%;	Pred. No. 2.8e-24;			
	Matches 141;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Oy	1 ggaagtcgtcttaacgacgcgltgtcgactagtatattgccgcagcgtccgggttgcta 60					
Db	1531 GGAGGTGGTGCACAGCGCGTGCTGCCACTGAATTTCCCGCAGCGTCCGGGTCCCTTA 1590					
Oy	61 tcacctaatcttgttccccaccaccaataagttaaacgttgtttaatgggttacca 120					
Db	1591 TCCCAGATTTCGTGCGCCCCGACCACAATAAGTTAAACGTGTGTTAATGGSTGCACCA 1650					
Oy	121 ggagcttatcgtgtttatat 141					
Db	1651 GGGCTTATCGTGTATTATAT 1671					
RESULT	6					
LOCUS	166494		7218 bp	DNA	linear	PAT 28-DEC -1997
DEFINITION	Sequence 14 from patent US 5670367.					
ACCESSION	166494					
VERSION	166494.1 GI:2724471					
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 7218)					
AUTHORS	Dorner,F., Scheffliner.F. and Falkner.F.Gunter.					
TITLE	Recombinant fowlpox virus					
JOURNAL	Patent: US 5670367-A 14-23-SEP-1997;					
FEATURES	Location/Qualifiers					
source	1..7218					
BASE COUNT	1944 a	1491 c	1486 g	1929 t	368 others	
ORIGIN						
Query Match	14.7%;	Score 73.4;	DB 6;	Length 7218;		
Best Local Similarity	7.6%;	Pred. No. 1.1e-07;				
Matches 29;	Conservative 213;	Mismatches 139;	Indels 0;	Gaps 0		
Oy	70 ttgcgtcggtcccgcagccaatagttaaacgttgtgtttatgtggtgacacagggtttat 129					
Db	1003 TTTCGTTTGCCANACGCTCACAGAATTAAITTCGAGCTTGCGCTGCAAGTCAAGGAGCTTG 1062					
Oy	130 cggtttatcatcgaatggcgaatttgtgcctccagtgtaattttgtatalcacaattaagtc 189					
Db	1063 CGATT 1122					
Oy	190 ttcttaactaatattttatcatccttttagttaagtcggtttgctgttttctgtc 249					



33473	36404:	contlg of 932 bp	in length
36405	36504:	gap of 100 bp	in length
36505	3734:	contlg of 930 bp	in length
37435	37534:	gap of 100 bp	in length
37535	38447:	contlg of 913 bp	in length
38448	38547:	gap of 100 bp	in length
38548	39476:	contlg of 929 bp	in length
39477	39576:	gap of 100 bp	in length
39577	40517:	contlg of 941 bp	in length
40518	41526:	contlg of 909 bp	in length
41527	41626:	gap of 100 bp	in length
41627	42519:	contlg of 893 bp	in length
42520	42619:	gap of 100 bp	in length
42620	43495:	contlg of 876 bp	in length
43496	43595:	gap of 100 bp	in length
43596	44503:	contlg of 908 bp	in length
44504	44603:	gap of 100 bp	in length
44589	44548:	contlg of 885 bp	in length
44589	46500:	contlg of 932 bp	in length
46521	46620:	gap of 100 bp	in length
46621	47557:	contlg of 917 bp	in length
47538	47657:	gap of 100 bp	in length
47638	48575:	contlg of 938 bp	in length
48576	48675:	gap of 100 bp	in length
48676	49600:	contlg of 925 bp	in length
49601	49700:	gap of 100 bp	in length
49701	50588:	contlg of 888 bp	in length
50589	50688:	gap of 100 bp	in length
50689	51624:	contlg of 936 bp	in length
51625	51724:	gap of 100 bp	in length
51725	52607:	contlg of 883 bp	in length
52608	52707:	gap of 100 bp	in length
52708	53630:	contlg of 923 bp	in length
53631	53730:	gap of 100 bp	in length
53731	54664:	contlg of 914 bp	in length
54665	54744:	gap of 100 bp	in length
54745	55704:	contlg of 960 bp	in length
55705	55804:	gap of 100 bp	in length
55805	56722:	contlg of 918 bp	in length
56723	56822:	gap of 100 bp	in length
56823	57739:	contlg of 917 bp	in length
57740	57839:	gap of 100 bp	in length
57840	58766:	contlg of 927 bp	in length
58767	58866:	gap of 100 bp	in length
58867	59775:	contlg of 909 bp	in length
59776	59875:	gap of 100 bp	in length
59876	60784:	contlg of 909 bp	in length
60785	60884:	gap of 100 bp	in length
60885	61795:	contlg of 911 bp	in length
61796	61895:	gap of 100 bp	in length
61896	62811:	contlg of 922 bp	in length
62818	62917:	gap of 100 bp	in length
62918	63841:	contlg of 924 bp	in length
63842	63941:	gap of 100 bp	in length
63942	64851:	contlg of 910 bp	in length
64852	64951:	gap of 100 bp	in length
64952	65844:	contlg of 897 bp	in length
65845	65948:	gap of 100 bp	in length
65949	66855:	contlg of 911 bp	in length
66860	66959:	gap of 100 bp	in length
66960	67875:	contlg of 916 bp	in length
67876	67975:	gap of 100 bp	in length
67977	68873:	contlg of 904 bp	in length
68880	68973:	gap of 100 bp	in length
68980	69907:	contlg of 928 bp	in length
69908	70007:	gap of 100 bp	in length
70008	70861:	contlg of 854 bp	in length
70862	70961:	gap of 100 bp	in length
70962	71880:	contlg of 919 bp	in length
71881	71980:	gap of 100 bp	in length
71981	72915:	contlg of 935 bp	in length

		72916	73015: gap of 100 bp	
	*	73016	73945: contig of 930 bp in length.	
Query Match		13.2%;	Score 66.2; DB 2: Length 156550;	
Best Local Similarity		46.6%;	Pred. No. 8.9e+06;	
Matches 152;	Conservative	0;	Mismatches 174; Indels 0; Gaps 0;	
QY	125	ttatcagcgtttatcatcgatgagcagtttgccctccagtgatatttggatataccaat	184	
DB	19603	TTNTTT	19662	
QY	185	aaggtttcctaccataatttatctttatcatcattcagtaagcgcggttgctcgtttc	244	
DB	19663	TT	19722	
QY	245	tgcgtcttcctcgtcggtcctccctcctcctcgttctcgttggtccaccatgcgcga	304	
DB	19723	TTTTNTTT	19782	
QY	305	tggcctataatgcgtatataataagacgagcttttcatgcgaagatcatccagtttg	364	
DB	19783	TT	19842	
QY	365	cttgaagccttctacttattacttcggttttcaacctatataacttggtttctt	424	
DB	19843	NTTTTTNTTTNTN	19902	
QY	425	tgatcggtttttctctcgtataact	450	
DB	19903	TNTTT	19928	

	<b>RESULT</b>	<b>8</b>
AC013349	AC013349	143585 bp DNA linear HTG 13-JUL-2000
LOCUS	Homo sapiens clone RP11-22K1, LOW-PASS SEQUENCE SAMPLING.	
DEFINITION	AC013349	
VERSION	AC013349.3 GI:9124043	
KEYWORDS	HTG; HTGS_PHASEO.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 143585)	
JOURNAL	Birren,B., Linton,L., Nussbaum,C. and Lander,E.	
REFERENCES	Homo sapiens, clone RPl1-22K1 Unpublished 2 (bases 1 to 143585) Birren,B., Linton,L., Nussbaum,C., Lander,E., Allen,N., Anderson,M. Baldin,J.J., Barua,N., Beckerly,R., Boguslavsky,L., Boukhalter.B., Brown,A., Castle.A., Colangelo.M., Collins,S., Collimore,A., Cooke,P., Deavellano,K., Dewar,K., Domino.M., Donelan.L., Doyle,M., Ferreira.P., Fitzhugh.W., Forrest.C., Funke.R., Gage,D., Galadyna,J., Gadnya.S., Grant,G., Hagos,B., Heatford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kahn,L., Karatas.A., Klein,T., Lewandzky,J., Lieu,C., Locke.K., Macdonald,P., Marquis.N., McEwan,P., McGurk.A., McKernan.K., McLaughlin,J., Meldrum,J., Morrow.J., Naylor,J., Norman.C.H., O'Connor.T., O'Donnell.P., Peterson,K., Pollara.V., Riley.R., Roy.A., Santos.R., Severy,P., Stange-Thumann,N., Stojanovic,N., Sudramanian,A., Talamas,J., Testaye,S., Tirrell,A., Vassiliev,H., Vo-A., Wheeler,J., Wu,X., Wyman.D., Ye,W.J., Zimmer.A. and Zody,M.	
COMMENT	Submitted (06-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gl:6910730. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RM/Repeatmasker.html">http://ftp.genome.washington.edu/RM/Repeatmasker.html</a> Genome Center	

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: <http://www.seq.wi.mit.edu>

Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center Project name: L4134  
Center Clone name: 22\_K\_1  
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\* NOTE: This record contains 150 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be generich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 930: contig of 930 bp in length  
\* 931 1030: gap of 100 bp  
\* 1031 1955: contig of 925 bp in length  
\* 1956 2055: gap of 100 bp  
\* 2056 2959: contig of 904 bp in length  
\* 2960 3059: gap of 100 bp  
\* 3060 4006: contig of 947 bp in length  
\* 4007 4106: gap of 100 bp  
\* 4107 4966: contig of 860 bp in length  
\* 4967 5066: gap of 100 bp  
\* 5067 5944: contig of 878 bp in length  
\* 5945 6044: gap of 100 bp  
\* 6045 6906: contig of 862 bp in length  
\* 6907 7006: gap of 100 bp  
\* 7007 7851: contig of 845 bp in length  
\* 7852 7951: gap of 100 bp  
\* 7952 8788: contig of 837 bp in length  
\* 8789 8888: gap of 100 bp  
\* 8889 9781: contig of 893 bp in length  
\* 9782 9881: gap of 100 bp  
\* 9882 10795: contig of 914 bp in length  
\* 10796 10895: gap of 100 bp  
\* 10896 11769: contig of 874 bp in length  
\* 11770 11869: gap of 100 bp  
\* 11870 12764: contig of 895 bp in length  
\* 12765 12864: gap of 100 bp  
\* 12865 13757: contig of 893 bp in length  
\* 13758 13857: gap of 100 bp  
\* 13858 14755: contig of 898 bp in length  
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[illegible]

Best Local Similarity 39.3%; Pred. No. 1.6e-05;  
Matches 128; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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Y  
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[illegible]

Y 365 ctgatagccttccacttattacttcgttttaacctataacttagttctt 424  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
O 48407 TTTTTTTTNNNTTTTTTTTTNNTNNNNTTTTTTTTTTTTNTT 48348

425 tgaacggtttttctctctgtatactt 450  
| | | | | | | | | | | |  
48347 TTNTTTTTTTTTTTNNNTTTTTTT 48322

ESULT	10		
DCUS			
2083839			
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DNA			
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TIME	02	00m	0000

DEFINITION	ACCSSION	VERSION	DESCRIPTION
Homo sapiens chromosome 8 clone RP11-179L5 map 8, LOW-PASS SEQUENCE SAMPLING.	AC083839	1	GT:10518397

SYNOPSIS	SYNOPSIS
HTG; HTGS_PHASE0.	HTG; HTGS_PHASE0.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 64789)  
Birren, B., Linton, L., Nussbaum, C. and Lander, E.  
Homo sapiens chromosome 8, clone RP11-17915  
TITLE

JOURNAL  
REFERENCE  
AUTHORS  
Unpublished  
2 (bases 1 to 64789)  
Birren, B., Linton, L., Nusbäum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Barna, N., Bastien, V., Beda, F., Rocusluykiv, I.

Boukngalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,  
Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,  
FitzHugh, W., Gage, D., Galagan, T., Gardner, S., Ginde, S., Govetto, M.

Graham, L., Grand-Pierre, N., Hagos, B., Heatford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Larocque, K., Lamazares, R., Landers, T., Lehoczyk, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, D., McKernan, V.

McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mienga, V.,  
Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T.,  
O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K.,  
Pierre, N., Pisani, C., Pollara, Raymond C., Rich, M., Ritz, D.

Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,  
Soutenez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
Tirrell, A., Travers, M., Trivelpiece, T., Vaccaro, N., Wald, D., and

WILSON, B., WU, X., WYMAN, D., YE, W.-J., YOUNG, G., ZAINOUBI, J.,  
ZIMMER, A. and ZODY, M.  
Direct Submission  
Submitted (03-OCT-2000) wh4tchop3@trestle.tulane.edu

Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.cse.cornell.edu/pub/RepeatMasker/>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR  
Web site: <http://www.seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
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Project Information  
Center project name: L11300  
Center clone name: j79\_L\_5

\* NOTE: This record contains 81 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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\* 9571 9670: gap of 100 bp  
\* 9671 10390: contig of 720 bp in length  
\* 10391 10490: gap of 100 bp  
\* 10491 11192: contig of 702 bp in length  
\* 11193 11292: gap of 100 bp  
\* 11293 11989: contig of 697 bp in length  
\* 11990 12089: gap of 100 bp  
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REFERENCE	artificial sequence.			
AUTHORS	1 (sites)			
TITLE	Olek A., Piepenbrock C. and Berlin K.			
JOURNAL	Diagnosis of diseases associated with the immune system			
FEATURES	Patent: WO 0200928-A 1670 03-JAN-2002;			
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VERSION	AL359957.31 GI:18476603			
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	1 (sites)			
JOURNAL	Chapman J.			
	Direct Submission			
	Submitted (29-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,			
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries:			
	humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk			
	On Feb 1, 2002 this sequence version replaced gi:18151457.			
	----- genome center			
	Center: Wellcome Trust Sanger Institute			
	Center code: SC			
	Web site: http://www.sanger.ac.uk			
	Contact: humquerry@sanger.ac.uk			
	----- Project Information			
	Center project name: ba62022			
	----- Summary Statistics			
	Assembly program: XGAP4; version 4.5			
	Sequencing vector: M13; M77815; 2% of reads			

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Sequencing vector: plasmid; 108752, 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 193212 bases at least Q40
Consensus quality: 193979 bases at least Q30
Consensus quality: 194657 bases at least Q20
Insert size: 195602; sum-of-contigs
Insert size: 189734; 3.2% error; agarose-1p
Quality coverage: 8.66x in Q20 bases; sum-of-contigs quality
coverage: 9.19x in Q20 bases; agarose-1p
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*	26099	26198:	gap of 100 bp	
*	26199	27086:	contlg of 888 bp	in length
*	27087	27186:	gap of 100 bp	
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*	40587	40686:	gap of 100 bp	
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*	41578	41677:	gap of 100 bp	
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*	56192	56291:	gap of 100 bp	
*	56292	57136:	contlg of 845 bp	in length
*	57137	57236:	gap of 100 bp	
*	57237	58132:	contlg of 896 bp	in length
*	58133	58232:	gap of 100 bp	
*	58233	59105:	contlg of 873 bp	in length
*	59106	59205:	gap of 100 bp	
*	59206	60078:	contlg of 873 bp	in length
*	60079	60178:	gap of 100 bp	
*	60179	61042:	contlg of 864 bp	in length

Query Match	Best Local Similarity	12.7%;	Score 63.4;	DB 2;	Length 83440;
Matches 148;	Conservative	0;	Mismatches 178;	Indels	Gaps 0;
QY 125	tttaccgtgtttataatcgatgcgcatgtgtgcctccagctgattttgtatataccaatt	184			
Db 45954	TTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT	46013			
QY 185	aaggttcttaccctaatttattttatcaatcttaagtaatgcggttgcctcgtttc	244			
Db 46014	TTTTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT	46073			
QY 245	tgcctgtcttcgtcggttcctctcctctcctcgtttcttcgtgttcctccatgcgcga	304			
Db 46074	TNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT	46133			
QY 305	tgggcttatagcgcatataatagacgagcttttaacgtcgaagatcatcagttg	364			
Db 46134	TTTTTNTTTTNTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT	46193			
QY 365	cttgatagccttctacacttattacttcgttttaacctctatacttgaatttctt	424			
Db 46194	TTTTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT	46253			
QY 425	tgcacggttttttctcgtatactt	450			
Db 46254	TTTTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT	46279			

RESULT 15	AC106848	8087 bp	DNA	linear	HTG 12-JAN-2002
LOCUS	AC106848/C				
DEFINITION	Homo sapiens chromosome 8 clone CTD-3149B6 map 8, LOW-PASS SEQUENCE				
ACCESSION	AC106848				
VERSION	AC106848.1				
KEYWORDS	HTG; HTGS-PHASE0.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Bitren,B., Linton,L., Nusbaum,C. and Lander,E.				
TITLE	1 (bases 1 to 8087)				
JOURNAL	Homo sapiens chromosome 8, clone CTD-3149B6				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 8087)				
Bitren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barina,N., Bastien,P., Boguslavsky,L., Boukhalter,B., Brown,A., Camarata,J., Campobello,A., Chang,J., Chazaro,B., Choebel,Y., Colangelo,M., Collins,S., Collymore,B., Cook,A., Cooke,P., DeRellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hades,B., Hefford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R., Landers,T., Lehoccky,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,C., Margus,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPherson,R., Melidrin,I.,					







